

Claims:

1. An isolated polynucleotide comprising a sequence selected from the group consisting of: consisting of: (1) sequences recited in SEQ ID NOS: 1-591, 1183-1912 and 1931-2106; (2) complements of the sequences recited in SEQ ID NOS: 1-591, 1183-1912 and 1931-2106; (3) reverse complements of the sequences recited in SEQ ID NOS: 1-591, 1183-1912 and 1931-2106; (4) reverse sequences of the sequences recited in SEQ ID NOS: 1-591, 1183-1912 and 1931-2106; (5) nucleotide sequences producing an Expectation ("E") value of 0.01 or less when compared to a sequence recited in (1) – (4) above; (6) nucleotide sequences having at least 50% identity to a nucleotide sequence recited in (1) – (4) above determined using computer algorithm BLASTN; (7) nucleotide sequences having at least 75% identity to a nucleotide sequence recited in (1) – (4) above determined using computer algorithm BLASTN; (8) nucleotide sequences having at least 90% identity to a nucleotide sequence recited in (1) – (4) above determined using computer algorithm BLASTN; (9) nucleotide sequences that hybridize to a sequence recited in (1) – (4) above under stringent hybridization conditions; (10) nucleotide sequences that are 200-mers of a sequence recited in (1) – (4) above; (11) nucleotide sequences that are 100-mers of a sequence recited in (1) – (4) above; (12) nucleotide sequences that are 40-mers of a sequence recited in (1) – (4) above; (13) nucleotide sequences that are 20-mers of a sequence recited in (1) – (4) above; and (14) nucleotide sequences that are degeneratively equivalent to a sequence recited in (1) – (4) above.
2. An oligonucleotide probe or primer comprising at least 10 contiguous residues complementary to 10 contiguous residues of a nucleotide sequence recited in claim 1.
3. An isolated polypeptide encoded by a polynucleotide according to claim 1.
4. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of: (a) sequences recited in SEQ ID NO: 592, 594-850, 852-930, 932-951, 953-1046, 1048-1182, 1913-1930, 2107-2293 and 2296-2368; (b) sequences having at least 60% identity to a sequence of SEQ ID NO: 592, 594-850, 852-930, 932-951, 953-1046, 1048-1182, 1913-1930, 2107-2293 and 2296-2368; (c) sequences having at least 90% identity to a sequence of SEQ ID NO: 592, 594-850, 852-930, 932-951,

953-1046, 1048-1182, 1913-1930, 2107-2293 and 2296-2368; and (d) sequences having at least 95% identity to a sequence of SEQ ID NO: 592, 594-850, 852-930, 932-951, 953-1046, 1048-1182, 1913-1930, 2107-2293 and 2296-2368.

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5. An isolated polynucleotide that encodes a polypeptide according to any one of claims 3 and 4.
6. A DNA construct comprising a polynucleotide according to any one of claims 1 and 5.

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7. A transgenic cell comprising a DNA construct according to claim 6.

8. A DNA construct comprising, in the 5'-3' direction:

- (a) a gene promoter sequence,
- (b) an open reading frame coding for at least a functional portion of a polypeptide of any one of claims 3 and 4; and
- (c) a gene termination sequence.

9. The DNA construct of claim 8 wherein the open reading frame is in a sense orientation.

10. The DNA construct of claim 8 wherein the open reading frame is in an antisense orientation.

11. The DNA construct of claim 8 wherein the gene promoter sequence and gene termination sequences are functional in a plant host.

12. The DNA construct of claim 8 further comprising a marker for identification of transformed cells.

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13. A DNA construct comprising, in the 5'-3' direction:

- (a) a gene promoter sequence,
- (b) an untranslated region of an isolated polynucleotide of any one of claims 1 and 5; and
- (c) a gene termination sequence.

14. The DNA construct of claim 13 wherein the untranslated region is in a sense orientation.

15. The DNA construct of claim 13 wherein the untranslated region is in an antisense orientation.

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16. The DNA construct of claim 13 wherein the gene promoter sequence and gene termination sequences are functional in a plant host.
17. A transgenic plant cell comprising a DNA construct of any one of claims 8 and 13.
18. A plant comprising a transgenic plant cell according to claim 17, or fruit or seeds or propagules thereof.
19. The plant of claim 18 wherein the plant is a woody plant.
20. The plant of claim 19 wherein the plant is selected from the group consisting of eucalyptus, pine, acacia, poplar, sweetgum, teak and mahogany species
21. A method for modifying gene expression in a plant comprising stably incorporating into the genome of the plant a DNA construct according to any one of claims 8 and 13.
22. The method of claim 21, wherein the plant is a woody plant.
23. The method of claim 21, wherein the plant is selected from the group consisting of eucalyptus, pine, acacia, poplar, sweetgum, teak and mahogany species.
24. A method for producing a plant having modified gene expression comprising:
 - (a) transforming a plant cell with a DNA construct according to any one of claims 8 and 13 to provide a transgenic cell; and
 - (b) cultivating the transgenic cell under conditions conducive to regeneration and mature plant growth.
25. The method of claim 24 wherein the plant is a woody plant.
26. The method of claim 24 wherein the plant is selected from the group consisting of eucalyptus, pine, acacia, poplar, sweetgum, teak and mahogany species.
27. A method for modifying the activity of a polypeptide in a plant comprising stably incorporating into the genome of the plant a DNA construct according to any one of claims 8 and 13.
28. The method of claim 27 wherein the plant is a woody plant.
29. The method of claim 27 wherein the plant is selected from the group consisting of eucalyptus, pine, acacia, poplar, sweetgum, teak and mahogany species.
30. An isolated polypeptide comprising a DNA-binding domain, wherein the DNA-binding domain comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 2279-2293 and 2296-2368.

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